

GenCore version 5.1.4.D5.4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 15:45:24 ; Search time 3.52121 Seconds

(without alignments)
977.656 Million cell updates/sec

Title: US-09-988-971-2_COPY_94_176

Sequence: 1 WLVEGLSRKAEKLELLPGN.....WLVSPLTLPQLQALVDHY 83

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_40:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	254	57.0	504	1	HCK_MACFA
2	254	57.0	504	1	HCK_HUMAN
3	242	54.3	511	1	LYN_HUMAN
4	241	54.0	503	1	HCK_RAT
5	241	54.0	511	1	LYN_MOUSE
6	241	54.0	511	1	LYN_RAT
7	240	53.8	524	1	HCK_MOUSE
8	232.5	52.1	504	1	HCK_HUMAN
9	228	51.1	508	1	HCK_HUMAN
10	227	50.9	508	1	HCK_MOUSE
11	224.5	50.3	498	1	BLK_MOUSE
12	223	50.0	507	1	LCK_CHICK
13	217	48.7	544	1	YES_XIPHE
14	215	48.2	537	1	YES_XENLA
15	214	48.0	541	1	YES_CHICK
16	212	47.5	529	1	FGF_HUMAN
17	212	47.5	543	1	YES_HUMAN
18	211	47.3	541	1	YES_MOUSE
19	210	47.1	517	1	FGF_MOUSE
20	209	46.9	533	1	LYN_MOUSE
21	207	46.4	528	1	YES_AVISY
22	207	46.4	545	1	FGF_FSVGR
23	206	46.2	533	1	FGF_CHICK
24	206	46.2	536	1	LYN_HUMAN
25	205	46.0	539	1	YES_CANPA
26	203	45.5	536	1	LYN_XENLA
27	197	44.2	536	1	LYN_XIPHE
28	195	43.7	535	1	YRK_CHICK
29	187	41.9	552	1	SRG1_DROME
30	186	41.7	526	1	SRG_AVISR
31	186	41.7	526	1	SRG_RSVSR
32	186	41.7	532	1	SRG_CHICK
33	186	41.7	557	1	SRG_AVISR

34	186	41.7	587	1	SRG_AVISR	P15054 avian sarco
35	185	41.5	566	1	SRG_AVISR	P14084 avian sarco
36	184.5	41.4	506	1	SRK4_SPOA	P42699 Spingilla 1
37	179	40.1	523	1	SRG_RSVPA	P31693 rous sarcom
38	177	39.7	526	1	SRG_RSVR	P00526 rous sarcom
39	177	39.7	535	1	SRG_HUMAN	P12931 homo sapien
40	177	39.7	535	1	SRG_RAT	Q9w4d9 ractus norv
41	177	39.7	540	1	SRG_MOUSE	P05480 mus muscu
42	176.5	39.6	496	1	SRM_MOUSE	O62270 mus muscu
43	173	38.8	531	1	SRG2_XENLA	P13116 xenopus lae
44	172	38.6	526	1	SRG_RSVH1	P25020 rous sarcom
45	171.5	38.5	509	1	STK_HYDAT	P17713 hydra atten

ALIGNMENTS

RESULT 1	HCK_MACFA	STANDARD	PRT	504 AA.
ID	HCK_MACFA			
AC	Q95M30			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK) (Hemopoietic cell kinase).			
GN	HCK.			
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;			
OC	Cercopithecoidea; Macaca.			
OX	NCBI_Taxid=9541;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Picard C.;			
RL	Thesis (2001), University of Marseille, France.			
CC	- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC			
CC	RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO			
CC	CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE			
CC	DEGRANULATION PROCESS OF NEUTROPHILS (By similarity).			
CC	- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein			
CC	tyrosine phosphate.			
CC	- SUBCELLULAR LOCATION: Membrane-associated (By similarity).			
CC	- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC			
CC	SUBFAMILY.			
CC	- SIMILARITY: CONTAINS 1 SH2 DOMAIN.			
CC	- SIMILARITY: CONTAINS 1 SH3 DOMAIN.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
DR	EMBL; AJ320181; CAC44031.1; -			
DR	InterPro; IPR000719; Euk_pkinase.			
DR	InterPro; IPR000980; SH2.			
DR	InterPro; IPR001452; SH3.			
DR	InterPro; IPR001245; Tyr_kinase.			
DR	Pfam; PF00017; SH2; 1.			
DR	Pfam; PF00018; SH3; 1.			
DR	Pfam; PF00069; pkinase; 1.			
DR	ProDom; PD000001; Euk_pkinase; 1.			
DR	ProDom; PD000066; SH3; 1.			
DR	ProDom; PD000093; SH2; 1.			
DR	ProSite; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	ProSite; PS00109; PROTEIN_KINASE_TYR; 1.			
DR	ProSite; PS00111; PROTEIN_KINASE_DOM; 1.			
DR	ProSite; PS00001; SH2; 1.			
DR	ProSite; PS00002; SH3; 1.			
DR	Transferrase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;			
KW				

KM Myristate; SH2 domain; SH3 domain.
 FT DOMAIN 56 116 SH3.
 FT DOMAIN 122 219 SH3.
 FT DOMAIN 240 493 PROTEIN KINASE.
 FT NP BIND 246 254 APP (BY SIMILARITY).
 FT BINDING 268 268 APP (BY SIMILARITY).
 FT ACT SITE 359 359 BY SIMILARITY.
 FT LIFT 2 2 MYRISTATE (BY SIMILARITY).
 FT MOD_RES 389 389 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 504 AA; 57096 MW; 53829322D2DE3423 CRC64;
 Query Match 57.0%; Score 254; DB 1; Length 504;
 Best Local Similarity 57.8%; Pred. No. 1.7e-22;
 Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
 QY 1 WLYEGLSRKAEELLPLPGNGAFPLRSQTRRSYSLSVRLSRPASWDRIRHRLHCL 60
 DB 122 WFFGIGSRKDAERQLAPGNLGSFMRISSETTKYSLSVRYDPRQGVKHKYKIRTL 181
 QY 61 DNGWLYISPLTLPPLQALVDHY 83
 DB 182 DNGGFYISPRSTFSTLQELVDHY 204
 RESULT 2
 HCK_HUMAN STANDARD; PRT; 526 AA.
 ID P08631; Q96C00; Q9H5Y5; Q9NUA4; Q9UMJ5;
 AC 01-AUG-1988 (Rel. 08, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P59-HCK and P60-HCK)
 DE (hemopoietic cell kinase).
 GN HCK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RX SEQUENCE OF 22-526 FROM N.A.
 RA MEDLINE=87257942; PubMed=3456523;
 RA Quintrell N., Lebo R., Varmus H., Bishop J.M., Petteinati M.J.,
 RA le Beau M.M., Diaz M.O., Rowley J.D.;
 RA "Identification of a human gene (HCK) that encodes a protein-tyrosine
 RT kinase and is expressed in hemopoietic cells.";
 RL Mol. Cell. Biol. 7:2267-2275(1987).
 RN [2]
 RX SEQUENCE OF 22-526 FROM N.A.
 RA MEDLINE=87257943; PubMed=3453117;
 RA Ziegler S.F., March J.D., Lewis D.B., Perlmutter R.M.;
 RT "Novel protein-tyrosine kinase gene (hck) preferentially expressed in
 RT cells of hematopoietic origin.";
 RL Mol. Cell. Biol. 7:2276-2285(1987).
 RN [3]
 RX SEQUENCE OF 22-526 FROM N.A.
 RA TISSUE=B-cell;
 RA Straussberg R.;
 RL Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RX SEQUENCE OF 22-526 FROM N.A.
 RC TISSUE=ileal mucosa;
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota C., Suzuki Y.,
 RA Ohsayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
 RA Iwagaki T., Sugano S.;
 RT "MEDO human cDNA sequencing project.";
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RX SEQUENCE FROM N.A.
 RA MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggaley C.L.,
 RA Bailey J., Bartlow K.F., Bates K.N., Beard L.M., Beate D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Frazer A., French L., Garner P.,
 RA Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Humble E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levasalho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McIay K., McMuray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.T.,
 RA Phillimore B.J.C.T., Prichardlingam S.R., Plund R.W., Ramsey H.,
 RA Rice C.M., Robe M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilmings L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871(2001).
 RN [6]
 RX SEQUENCE OF 179-526 FROM N.A.
 RA TISSUE=Spleen;
 RX MEDLINE=92241680; PubMed=1572549;
 RA Haderitzky D., Streibhardt K., Ruegenen-Waigmann H.;
 RT "The genomic locus of the human hemopoietic-specific cell protein
 RT tyrosine kinase (PTK) encoding gene (HCK) confirms conservation of
 RT exon-intron structure among human PTKs of the src family.";
 RL Gene 113:275-280(1992).
 RN [7]
 RX SEQUENCE OF 1-22 FROM N.A., AND ALTERNATIVE INITIATION.
 RA MEDLINE=91342636; PubMed=1875927;
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsey R., Dunn A.R.;
 RT "Two isoforms of murine hck, generated by utilization of alternative
 RT translational initiation codons, exhibit different patterns of
 RT subcellular localization.";
 RL Mol. Cell. Biol. 11:4363-4370(1991).
 RN [8]
 RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 78-526.
 RA MEDLINE=97177106; PubMed=9024658;
 RA Slicheri F., Moareff J., Kurtyan J.;
 RT "Crystal structure of the Src family tyrosine kinase Hck.";
 RL Nature 385:602-609(1997).
 RN [9]
 RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 81-137.
 RA MEDLINE=98453315; PubMed=9778343;
 RA Arold S., O'Brien R., Franken P., Strub M.P., Hoh F., Dumas C.,
 RA Labbury J.E.;
 RT "RT loop flexibility enhances the specificity of Src family SH3
 RT domains for HIV-1 Nef.";
 RL Biochemistry 37:14683-14691(1998).
 RN [10]
 RX STRUCTURE BY NMR OF 78-138.
 RA MEDLINE=98239731; PubMed=9571048;
 RA Horita D.A., Baldesseri D.M., Zhang W., Altieri A.S., Smithgall T.E.,
 RA Gmeiner W.H., Byrd R.A.;
 RT "Solution structure of the human Hck SH3 domain and identification of
 RT its ligand binding site.";
 RL J. Mol. Biol. 278:253-265(1998).
 RN [11]
 RX STRUCTURE BY NMR OF 139-245.
 RA MEDLINE=97263487; PubMed=9109402;
 RA Zhang W., Smithgall T.E., Gmeiner W.H.;
 RT "Sequential assignment and secondary structure determination for the
 RT Src homology 2 domain of hematopoietic cellular kinase.";
 RL FEBS Lett 406:131-135(1997).
 CC - FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE PC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO

CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 DEGRANULATION PROCESS OF NEUTROPHILS.
 -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 -1- SUBCELLULAR LOCATION: P60-HCK AND P59-HCK ARE ASSOCIATED WITH
 MEMBRANES. P60-HCK IS ALSO CYTOPLASMIC (BY SIMILARITY).
 -1- ALTERNATIVE PRODUCTS: 2 isoforms, P60-HCK (shown here) and P59-
 HCK; are produced by alternative initiation.
 -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE
 MYELOID AND B-LYMPHOID LINEAGES.
 -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 SUBFAMILY.
 -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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 or send an email to license@isb-sib.ch).

 DR EMBL; M16591; AAA52643.1; -;
 DR EMBL; M16592; AAA52644.1; -;
 DR EMBL; BC014435; AAH14435.1; -;
 DR EMBL; AK026432; BAB15482.1; -;
 DR EMBL; AL049539; CAB75606.1; -;
 DR EMBL; X58741; CAA1565.2; -;
 DR EMBL; X58742; CAA1565.2; JOINED.
 DR EMBL; X58743; CAA1565.2; JOINED.
 DR PIR; A27812; TVHHC.
 DR PDB; 2HCK; 20-AUG-97.
 DR PDB; 3HCK; 15-OCT-97.
 DR PDB; 4HCK; 17-JUN-98.
 DR PDB; 5HCK; 17-JUN-98.
 DR PDB; 1AD5; 15-MAY-97.
 DR PDB; 1BU1; 11-NOV-98.
 DR Genew; HGNC:4840; HCK.
 DR MIM; 142370; -;
 DR Interpro; IPR000719; Euk_pkinase.
 DR Interpro; IPR000980; SH2.
 DR Interpro; IPR001452; SH3.
 DR Interpro; IPR002290; Ser_thr_pkinase.
 DR Interpro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 2.
 DR Pfam; PF00069; pkinase; 4.
 DR Prodom; PD000066; SH3; 1.
 DR Prodom; PD000093; SH2; 1.
 DR SMART; SM00352; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00220; S_TKc; 1.
 DR SMART; SM00219; TYKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR Transerbase; Tyrosine-protein kinase, Phosphorylation, ATP-binding;
 KW Tyristate; SH2 domain; SH3 domain; Alternative initiation;
 KW 3D-structure.
 FT CHAIN 1 526 TYROSINE-PROTEIN KINASE P60-HCK.
 FT INIT MET 22 526 TYROSINE-PROTEIN KINASE P59-HCK.
 FT DOMAIN 76 138 FOR ISOFORM P59-HCK.
 FT DOMAIN 144 241 SH2.
 FT DOMAIN 262 315 PROTEIN KINASE.
 FT NP_BIND 268 276 ATP.
 FT BINDING 290 290 ATP.
 FT ACT SITE 381 391 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 FT LIPID 23 23 MYRISTATE (BY SIMILARITY).

FT MOD RES 411 411 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CONFLICT 24 24 C -> S (IN REF. 1).
 FT CONFLICT 144 144 W -> R (IN REF. 4).
 SQ SEQUENCE 526 AA; 59599 MW; 847B877A0A41725 CRC64;
 Query Match 57.0%; Score 254; DB 1; Length 526;
 Best Local Similarity 57.8%; Pred. No. 1.8e-22;
 Matches 48; Conservative 13; Mismatches 22; Indels 0; Gaps 0;
 QY 1 MLYGKSPKAEKELLPGNGAFIPRESQRCGYSVLRSPASMDRIHRHICL 60
 DB 144 WFFGKSRKDAERQLAPGNLGSFMRKDSYTKSSISLVRYDPRQGVKHKIRTL 203
 QY 61 DNGWLYSPRLTFPSLQALVDHY 83
 DB 204 DNGGFYISPRSTFSTLQELVDHY 226
 RESULT 3
 LYN HUMAN
 ID LYN HUMAN STANDARD; PRT; 511 AA.
 AC P07948;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
 GN LYN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=67327210; PubMed=3561390;
 RA Yamashita Y., Fukushige S.-I., Semba K., Sukegawa J., Miyajima N.,
 RA Matsubara K.-I., Yamamoto T., Toyoshima K.;
 RT "The yes-related cellular gene lyn encodes a possible tyrosine kinase
 RT similar to p56lck.";
 RL Mol. Cell. Biol. 7:237-243(1987).
 RN [2]
 RP SEQUENCE FROM N. A.
 RX MEDLINE=94171041; PubMed=8125304;
 RA Rider L.G., Raben N., Miller L., Jelsema C.;
 RT "The cdnas encoding two forms of the lyn protein tyrosine kinase are
 RT expressed in rat mast cells and human myeloid cells.";
 RL Gene 138:219-222(1994).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 DR EMBL; M16038; AAA59540.1; -;
 DR EMBL; M79321; AAB50019.1; -;
 DR PIR; A26719; TVHULY.
 DR HSSP; P08631; 1AD5.
 DR Genew; HGNC:6735; LYN.
 DR MIM; 165120; -;
 DR Interpro; IPR000719; Euk_pkinase.
 DR Interpro; IPR000980; SH2.
 DR Interpro; IPR001452; SH3.
 DR Interpro; IPR001245; Tyr_pkinase.

DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_Pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT MET 0 BY SIMILARITY.
 FT LIPID 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 PALMITATE (BY SIMILARITY).
 FT DOMAIN 62 122 SH3.
 FT DOMAIN 128 225 SH2.
 FT DOMAIN 246 500 PROTEIN KINASE.
 FT NP BIND 252 260 ATP (BY SIMILARITY).
 FT BINDING 274 274 ATP (BY SIMILARITY).
 FT ACT SITE 366 366 BY SIMILARITY.
 FT MOD RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD RES 507 507 PHOSPHORYLATION (BY SIMILARITY).
 FT VARRESLIC 22 42 MISSING (IN ISOPORN LYN B).
 SQ SEQUENCE 511 AA; 58442 MW; 8419CD461204E364 CRC64;

Query Match 54.3%; Score 242; DB 1; Length 511;
 Best Local Similarity 54.2%; Pred. No. 4,6e-21;
 Matches 45; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLRLGNPGAFILRESQTRGYSISVRLSPASWDRIHRYHICL 60
 Db 128 WFFKDIIRKDAERHLLAPGNMGLSFMIRDSSETTKGYSISVRDPPQHGDTVGHYKIRTL 187

Qy 61 DNGMWLYSPRLTPPSLQALVDHY 83
 Db 188 DNGGYIISPRITPFCISDMIKHY 210

RESULT 4
 HCK_RAT STANDARD; PRT; 503 AA.

AC PS0545; Q64647;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK) (Hemopoietic cell
 kinase).
 GN HCK.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92109719; PubMed=1764064;
 RA Okano Y., Sugimoto Y., Fukuko M., Matsui A., Nagata K.I., Nozawa Y.,
 RT "Identification of rat cDNA encoding hck tyrosine kinase from
 RT megakaryocytes";
 RL Biochem. Biophys. Res. Commun. 181:1137-1144(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Wistar; TISSUE=Spleen;
 RA Vijaya Gouri B.S., Renu V., Kanakar S., Swarnup G.;
 RT "Nucleotide sequence of a cDNA coding for rat hck tyrosine kinase and
 RT characterization of its gene product.";

RL J. Biochem. 19:117-129(1994).
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Membrane-associated.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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 CC or send an email to license@isb-sib.ch).

DR EMBL; S74141; AAB20754.1; -;
 DR EMBL; M63666; AA41312.1; -;
 DR EMBL; X62345; CAA44218.1; -;
 DR HSSP; P08631; 1B01.
 DR InterPro; IPR000719; Euk_Pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001245; Tyr_Pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00401; SH3DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_Pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Transferase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
 KW Myristate; SH2 domain; SH3 domain.
 FT DOMAIN 55 115 SH3.
 FT DOMAIN 121 218 SH2.
 FT DOMAIN 239 492 PROTEIN KINASE.
 FT NP BIND 245 253 ATP (BY SIMILARITY).
 FT BINDING 267 267 ATP (BY SIMILARITY).
 FT ACT SITE 358 358 BY SIMILARITY.
 FT LIPID 2 MYRISTATE (BY SIMILARITY).
 FT MOD RES 388 388 F -> V (IN REF. 2).
 FT MOD RES 51 51 K -> R (IN REF. 2).
 FT CONFLICT 205 205 I -> T (IN REF. 2).
 FT CONFLICT 306 306
 SQ SEQUENCE 503 AA; 57016 MW; A1FC1F3F082EF73 CRC64;

Query Match 54.0%; Score 241; DB 1; Length 503;
 Best Local Similarity 56.6%; Pred. No. 5.9e-21;
 Matches 47; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

Qy 1 WLYEGLSREKAEELLRLGNPGAFILRESQTRGYSISVRLSPASWDRIHRYHICL 60
 Db 121 WFFKDIIRKDAERHLLAPGNMGLSFMIRDSSETTKGYSISVRDPPQHGDTVGHYKIRTL 180

Qy 61 DNGMWLYSPRLTPPSLQALVDHY 83
 Db 181 DSGGYIISPRITPFCISDMIKHY 203

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RESULT 5
LYN_MOUSE
ID LYN_MOUSE STANDARD; PRT; 511 AA.
AC P25911; Q62127;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
GN LYN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91260688; PubMed=1710766;
RA Stanley E., Ralph S.J., McEwen S., Boulet I., Holtzman D.A.,
RA Lock P., Dunn A.R.;
RT "Alternatively spliced murine lyn mRNAs encode distinct proteins.";
RL Mol. Cell. Biol. 11:3399-3406(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91203857; PubMed=2017160;
RA Yi T., Bolen J.B., Ihle J.N.;
RT "Hematopoietic cells express two forms of lyn kinase differing by 21
RT amino acids in the amino terminus.";
RL Mol. Cell. Biol. 11:2391-2396(1991).
RN [3]
RP SEQUENCE OF 363-431 FROM N.A.
RX MEDLINE=90152381; PubMed=2482828;
RA Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;
RT "The application of the polymerase chain reaction to cloning members
RT of the protein tyrosine kinase family.";
RL Gene 85:67-74(1989)
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, LYN A (SHOWN HERE) AND LYN B;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND
CC MYELOID CELLS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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CC -----
DR EMBL; M64608; AAA39470.1; -
DR EMBL; M57696; AAA39471.1; -
DR EMBL; M57697; AAA39472.1; -
DR EMBL; M33426; AAA40017.1; -
DR PIR; A39719; A39719.
DR HSSP; P08631; IADS.
DR MGD; MGI:96892; LYN.
DR InterPro; IPR000719; Euk_Pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_Pkinase.
DR Pfam; PF000017; SH2; 1.
DR Pfam; PF000018; SH3; 1.
DR Pfam; PF00069; Pkinase; 1.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_Pkinase; 1.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000093; SH2; 1.

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DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
KW Palmitate; Lipoprotein; Alternative splicing.
FT INTR. MET 0
FT INIT 1
FT LIPID 2
FT DOMAIN 62
FT DOMAIN 122
FT DOMAIN 128
FT DOMAIN 246
FT NP_BIND 252
FT BINDING 274
FT ACT_SITE 366
FT MOD_RES 396
FT MOD_RES 507
FT VARSPIC 24
FT CONFLICT 76
FT CONFLICT 160
FT CONFLICT 278
FT CONFLICT 390
FT CONFLICT 414
FT CONFLICT 424
FT CONFLICT 431
SQ SEQUENCE 511 AA; 58681 MW; 3935221C90C50F0 CRC64;
Query Match 54.0%; Score 241; DB 1; Length 511;
Best Local Similarity 54.2%; Pred. No. 6e-21;
Matches 45; Conservative 14; Mismatches 24; Indels 0; Gaps 0;
Qy 1 WLVEGLSRKAEELLPGNPGAFILRESQTRGSYSLSVRLSPASWDRIRYRTHCL 60
Db 128 WFFEDITRDADARQLAPGNSACAFILRESFTLKGSSLSVRDYMWDVYKIKYKRL 187
Qy 61 DNGMLYSPRLTFPSLQALVDHY 83
Db 188 DNGGYISPRITFPCISDMIKHY 210
RESULT 6
LYN_RAT
ID LYN_RAT STANDARD; PRT; 511 AA.
AC Q07014; Q63320;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
GN LYN.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Minoguchi K., Nishikata H., Stragantian R.P.;
RT "Bacterially expressed rat p56lyn binds several proteins in rat
RT basophilic leukemia cells including pp72, a tyrosine phosphorylated
RT protein prominent in activated cells.";
RL J. Immunol. 150:222-222(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94171041; PubMed=8125304;
RA Rider L.G., Raben N., Miller L., Jelsma C.;
RT "The cDNAs encoding two forms of the LYN protein tyrosine kinase are
RT expressed in rat mast cells and human myeloid cells.";
RL Gene 138:219-222(1994).
RN [3]

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RP SEQUENCE FROM N.A.
 RX MEDLINE=97442484; PubMed=9295361;
 RA Vonkles B.M., Chen H., Haleem-Smith H., Metzger H.;
 RT "The unique domain as the site on Lym kinase for its constitutive
 association with the high affinity receptor for IgE";
 RL J. Biol. Chem. 272:24072-24080(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND
 CC MYELOID CELLS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L14951; AAA41549.1; -;
 DR EMBL; L14782; AAA20944.1; -;
 DR EMBL; L14823; AAA20945.1; -;
 DR EMBL; AF0003100; AAB71344.1; -;
 DR EMBL; AF0003101; AAB71344.1; -;
 DR EMBL; AF0003102; AAB71346.1; -;
 DR HSSP; P08631; 1AD5.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; Tyr_pkinase.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF000017; SH2; 1.
 DR Pfam; PF000018; SH3; 1.
 DR Pfam; PF000059; pkinase; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferrase; ATP-binding; Wristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT MET 0
 FT LIPID 1
 FT LIPID 2
 FT LIPID 2
 FT DOMAIN 62 122
 FT DOMAIN 128 225
 FT DOMAIN 246 500
 FT NP BIND 252 260
 FT BINDING 274 274
 FT ACT SITE 366
 FT MOD RES 396
 FT MOD RES 507
 FT VARSPDLC 24 44
 FT CONFLACT 230 230
 FT CONFLACT 307 307
 FT CONFLICT 418 418
 SO SEQUENCE 511 AA; 58529 MW; 24425E229CD43ED CRC64;

Query Match

54.0%; Score 241; DB 1; Length 511;

Best Local Similarity 54.2%; Pred. No. 6e-21;
 Matches 45; Conservative 14; Mismatches 24; Indels 0; Gaps 0;
 QY 1 WLWGLSREKAEELLPLPNGCAFILRESQTRRSYSLSVRLSPASWDRIRHRIHCL 60
 DB 128 WFPDIDIRKNAEQGLAPGNSAGAFILRESLTKGSFSLSVROYDPMHGVKIKYKISL 187
 QY 61 DNGWLYSPLTPPLPSLQALVDHY 83
 DB 188 DNGWYISPLTPPTPTCSIMINHY 210
 RESULT 7
 HCK_MOUSE
 ID HCK_MOUSE STANDARD; PRT; 524 AA.
 AC P08103;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK and P60-HCK)
 DE (Hemopoietic cell kinase) (B-cell/myeloid kinase) (BMK).
 GN HCK
 OS Mus musculus (Mouse)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 22-524 FROM N.A.
 RC STRAIN=ICR; TISSUE=Macrophage;
 RC MEDLINE=88067781; PubMed=3684607;
 RA Klemes M.J., McKercher S.R., Maki R.A.;
 RT "Nucleotide sequence of the mouse hck gene";
 RL Nucleic Acids Res. 15:5600-5600(1987).
 RN [2]
 RP SEQUENCE OF 22-524 FROM N.A.
 RA MEDLINE=88068587; PubMed=3317404;
 RA Holtzman D.A., Cook W.D., Dunn A.R.;
 RT "Isolation and sequence of a cDNA corresponding to a src-related gene
 RT expressed in murine hemopoietic cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8325-8329(1987).
 RN [3]
 RP SEQUENCE OF 1-22 FROM N.A., AND ALTERNATIVE INITIATION.
 RX MEDLINE=91342636; PubMed=1875927;
 RA Lock P., Ralph S., Stanley E., Boulet I., Rameay R., Dunn A.R.;
 RT "Two isoforms of murine hck, generated by utilization of alternative
 RT translational initiation codons, exhibit different patterns of
 RT subcellular localization";
 RL Mol. Cell. Biol. 11:4363-4370(1991).
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: P59-HCK AND P56-HCK ARE ASSOCIATED WITH
 CC MEMBRANES. P59-HCK IS ALSO CYTOPLASMIC.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1959-HCK (shown here) and P56-
 CC HCK; are produced by alternative initiation.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE
 CC MYELOID AND B-LYMPHOID LINEAGES.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC -----

DR EMBL; Y00487; CAA68544.1; -;
 DR EMBL; J03023; AAA37305.1; -;
 DR PIR; A27282; TVMSHC.
 DR PIR; A39973; A39973.
 DR HSSP; P08631; IAD5.
 DR MGD; MGI:96052; HCK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH2DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR TRANSFERASE; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
 KM Myristate; SH2 domain; SH3 domain; Alternating initiation.
 FT CHAIN 1 524 TYROSINE-PROTEIN KINASE P59-HCK.
 FT INIT MET 22 524 TYROSINE-PROTEIN KINASE P56-HCK.
 FT DOMAIN 22 22 FOR ISOFORM P56-HCK.
 FT DOMAIN 142 239 SH2.
 FT DOMAIN 260 513 PROTEIN KINASE.
 FT NP BIND 266 274 ATP (BY SIMILARITY).
 FT BINDING 288 288 ATP (BY SIMILARITY).
 FT ACT SITE 379 379 BY SIMILARITY.
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 FT LIPID 23 23 MYRISTATE (BY SIMILARITY).
 FT MOD RES 409 409 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 524 AA; 59129 MW; DF72PDS9B38C9706 CRC64;

Query Match 53.8%; Score 240; DB 1; Length 524;
 Best Local Similarity 56.6%; Pred. No. 8.1e-21;
 Matches 47; Conservative 13; Mismatches 23; Indels 0; Gaps 0;

QY 1 WYEGLSPEKAEELLIPNPGCAFLESQTRGYSLSVLSPPASWPRIRHRIHCL 60
 DB 142 WPKGISKQKHEHLLAPGNMIGSMINDSTTKGYSLSVDPDPQHGDTVGHYKIRTL 201

QY 61 DNGWLISPRITPESLQALVDHY 83
 DB 202 DSGGFYISPRSTFSSLOELVLHY 224

RESULT 8
 ID BLK_HUMAN STANDARD; PRT; 504 AA.
 AC P51451; Q16291;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase Blk (EC 2.7.1.112) (B lymphocyte kinase) (p55-
 DE BLK).
 GN BLK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RN MEDLINE=9512307B; PubMed=7822795;

RA Islam K.B., Rabhani H., Larsson C., Sanders R., Smith C.I.;
 RT "Molecular cloning, characterization, and chromosomal localization of
 RT a human lymphoid tyrosine kinase related to murine Blk.";
 RL J. Immunol. 154:1265-1272 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95148218; PubMed=7845672;
 RA Drebin J.A., Hartzell S.W., Griffin C., Campbell M.J.;
 RT "Molecular cloning and chromosomal localization of the human homologue
 RT of a B-lymphocyte specific protein tyrosine kinase (blk).";
 RL Oncogene 10:477-486 (1995).
 CC -1- FUNCTION: BLK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT
 CC IS RESTRICTED TO B LYMPHOID CELLS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL; Z3398; CAA83965.1; -;
 DR EMBL; Z76617; AAB3365.1; -;
 DR HSSP; P16277; BLK.
 DR GENE; HGNC:1057; BLK.
 DR MIM; 191305; -;
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH2DOMAIN.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TyKc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; FALSE_NEG.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50002; SH3; 1.
 DR Tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding;
 KM Myristate; SH2 domain; SH3 domain.
 FT INIT MET 0 0 BY SIMILARITY.
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 57 117 SH3.
 FT DOMAIN 123 219 SH2.
 FT DOMAIN 240 493 PROTEIN KINASE.
 FT NP BIND 246 254 ATP (BY SIMILARITY).
 FT BINDING 268 268 ATP (BY SIMILARITY).
 FT ACT SITE 359 359 BY SIMILARITY.
 FT MOD RES 388 388 M -> V (IN REF. 2).
 FT CONFLICT 286 286 I -> Y (IN REF. 2).
 FT CONFLICT 406 406 I -> Y (IN REF. 2).
 SQ SEQUENCE 504 AA; 57607 MW; BDB1DF50BC7370C8 CRC64;

Query Match 52.1%; Score 232.5; DB 1; Length 504;
 Best Local Similarity 54.2%; Pred. No. 6e-20;
 Matches 45; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

OY 1 WYEGSLREKAEELLPPNPGAFIRESSOTRSGYSLSVLRSPASWDRIKRRHCHC 60
DB 123 WFRSQCKEAEKRLAPINAKASFILRESEINKGAFSLSVK-DVTTQCELIKHKIRCL 181
OY 61 DNGWLYSPRLTPPSLQALVDHY 83
DB 182 DEGYXISPRITFSLQALVQHY 204

RESULT 9
LCK_HUMAN
ID LCK_HUMAN STANDARD; PRT: 508 AA.
AC P06239; P07100; Q9NTT8; Q96DW4; Q13152; Q12850;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase LCK (BC 2.7.1.112) (P56-LCK)
DE (LSK) (T cell-specific protein-tyrosine kinase).
GN LCK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RX MEDLINE=89123626; PubMed=3265417;
RA Perlmuter R.M., March J.D., Lewis D.B., Peet R., Ziegler S.F.,
RA Wilson C.B.,
RT "structure and expression of lck transcripts in human lymphoid
RT cells";
RL J. Cell. Biochem. 38:117-126(1988).
RN 12
RP SEQUENCE FROM N.A.
RX MEDLINE=87133831; PubMed=3493153;
RA Koga Y., Caccia N., Toyonaga B., Spolski R., Yanagi Y., Yoshikai Y.,
RA Mak T.W.,
RT "A human T cell-specific cDNA clone (Y116) encodes a protein with
RT extensive homology to a family of protein-tyrosine kinases";
RL Eur. J. Immunol. 16:1643-1646(1986).
RN 13
RP SEQUENCE FROM N.A.
RX MEDLINE=90108697; PubMed=2558056;
RA Rouer E., Van Huynh T., de Souza S.L., Lang M.C., Fischer S.,
RA Benarous R.,
RT "structure of the human lck gene: differences in genomic organisation
RT within src-related genes affect only N-terminal exons";
RL Gene 84:105-113(1983).
RN 14
RP SEQUENCE FROM N.A., VARIANTS L-27, POKP-231 INS, V-352, L-446, AND
RP PHOSPHORYLATION OF TYR-393 AND TYR-504.
RC TISSUE=Leukemia;
RX MEDLINE=94187714; PubMed=8139546;
RA Wright D.D., Sefton B.M., Kamps M.P.,
RT "oncogenic activation of the lck protein accompanies translocation of
RT the lck gene in the human HSB2 T-cell leukemia";
RL Mol. Cell. Biol. 13:2429-2437(1993).
RN 15
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Leukemic T-cell;
RX MEDLINE=96085119; PubMed=7495859;
RA Vogel L.B., Arthur R., Fujita D.J.,
RT "an aberrant lck mRNA in two human T-cell lines";
RL Biochim. Biophys. Acta 1264:168-172(1995).
RN 16
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.,
RT Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
RN 17
RP SEQUENCE OF 13-508 FROM N.A.
RC TISSUE=Peritoneal blood lymphocytes;
RX MEDLINE=20462621; PubMed=11009097;
RA Boncristiano M., Majolini M.B., D'Elia M.M., Pacini S., Valensin S.,
RA Uivieri C., Amedei A., Falini B., Del Prete G., Telford J.L.,
RA Balderi C.T.,
RT "Defective recruitment and activation of ZAP-70 in common variable
RT immunodeficiency patients with T cell defects";
RL Eur. J. Immunol. 30:2632-2638(2000).
RN 18
RP SEQUENCE OF 367-508 FROM N.A.
RX MEDLINE=88217332; PubMed=2835736;
RA Vellente A., Rose F.M., Sawville E.A., Bojen J.B., Rosen N.,
RT "Expression of the lck tyrosine kinase gene in human colon carcinoma
RT and other non-lymphoid human tumor cell lines";
RL Oncogene Res. 1:357-374(1987).
RN 19
RP SEQUENCE OF 374-508 FROM N.A.
RX MEDLINE=87000726; PubMed=3489486;
RA Trevillian J.M., Lin Y., Chen S.J., Phillips C.A., Canna C.,
RA Lima T.J.,
RT "Human T lymphocytes express a protein-tyrosine kinase homologous to
RT p56LCK";
RL Biochim. Biophys. Acta 888:286-295(1986).
RN 10
RP SEQUENCE OF 1-34 FROM N.A.
RX MEDLINE=89096891; PubMed=2850479;
RA Garvin A.M., Pawar S., March J.D., Perlmuter R.M.,
RT "structure of the murine lck gene and its rearrangement in a murine
RT lymphoma cell line";
RL Mol. Cell. Biol. 8:3058-3064(1988).
RN 11
RP SEQUENCE OF 1-34 FROM N.A.
RX MEDLINE=89131764; PubMed=2787474;
RA Takadera T., Leung S., Gernone A., Koga Y., Takihara Y.,
RA Miyamoto N.G., Mak T.W.,
RT "structure of the two promoters of the human lck gene: differential
RT accumulation of two classes of lck transcripts in T cells";
RL Mol. Cell. Biol. 9:2173-2180(1989).
RN 12
RP MASS SPECTROMETRY.
RC TISSUE=Breast cancer;
RX MEDLINE=21829512; PubMed=11840567;
RA Harris R.A., Yang A., Stein R.C., Lucy K., Brusten L., Herath A.,
RA Parekh R., Waterfield M.D., O'Hare M.J., Neville M.A., Page M.J.,
RA Zvelebil M.J.,
RT "Cluster analysis of an extensive human breast cancer cell line
RT protein expression map database";
RL Proteomics 2:212-223(2002).
RN 13
RP INTERACTION WITH PI3K.
RX MEDLINE=94067101; PubMed=7504174;
RA Vogel L.B., Fujita D.J.,
RT "The SH3 domain of p56lck is involved in binding to
RT phosphatidylinositol 3'-kinase from T lymphocytes";
RL Mol. Cell. Biol. 13:7408-7417(1993).
RN 14
RP INTERACTION WITH KHDRBS1.
RX MEDLINE=95153508; PubMed=7852312;
RA Vogel L.B., Fujita D.J.,
RT "p70 phosphorylation and binding to p56lck is an early event in
RT interleukin-2-induced onset of cell cycle progression in
RT T-lymphocytes";
RL J. Biol. Chem. 270:2506-2511(1995).
RN 15
RP PHOSPHORYLATION OF TYR-504.
RX MEDLINE=92347326; PubMed=1639064;
RA Bergman M., Mustelin T., Oetken C., Partanen J., Flint N.A.,
RA Amrein K.E., Autero M., Burn P., Allitalo K.,
RT "The human p50csk tyrosine kinase phosphorylates p56lck at Tyr-505 and
RT down regulates its catalytic activity";
RL EMBO J. 11:2919-2924(1992).
RN 16
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 52-225.
RX MEDLINE=94203291; PubMed=7512222;
RA Eck M.J., Atweell S.K., Shoelson S.E., Harrison S.C.;

[illegible]

RA Abraham K.M., Levin S.D., March J.D., Forbush K.A., Perlmuter R.M.,
 RT "Thymic tumorigenesis induced by overexpression of p56lck.",
 RL Proc. Natl. Acad. Sci. U.S.A. 88:3977-3981(1991).
 RN [9]
 RP MUTAGENESIS.
 RX MEDLINE=93133805; PubMed=8421674;
 RA Carrera A.C., Alexandrov K., Roberts T.M.;
 RT "The conserved lysine of the catalytic domain of protein kinases is
 RT actively involved in the phosphotransfer reaction and not required
 RT for anchoring ATP.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:442-446(1993).
 RN [10]
 RP PALMITOYLATION
 RX MEDLINE=94019312; PubMed=8412237;
 RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;
 RT "Palmitoylation of an amino-terminal cysteine motif of protein
 RT tyrosine kinases p56lck and p59fyn mediates interaction with
 RT glycosyl-phosphatidylinositol-anchored proteins.";
 RL Mol. Cell. Biol. 13:6385-6392(1993).
 RN [11]
 RP PALMITOYLATION
 RX MEDLINE=95071286; PubMed=7980442;
 RA Koege M., Zlatkine P., Ley S.C., Courtenidge S.A., Magee A.I.;
 RT "Palmitoylation of multiple Src-family kinases at a homologous N-
 RT terminal motif.";
 RL Biochem. J. 303:749-753(1994).
 CC -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
 CC ITS EARLY EXPRESSION IS ESSENTIAL FOR EARLY T-LYMPHOCYTE
 CC DEVELOPMENT.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER
 CC CD4 OR CD8.
 CC -1- TISSUE SPECIFICITY: PRESENT AT A LOW LEVEL IN MOST T CELLS, AND
 CC AT AN ELEVATED LEVEL IN LSTRA AND THY 19 (T-CELL LYMPHOMA) CELLS.
 CC -1- DEVELOPMENTAL STAGE: LEVELS REMAIN RELATIVELY CONSTANT THROUGHOUT
 CC T-CELL ONTOGENY.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC -----
 DR EMBL: X03533; CAA27234.1; -
 DR EMBL: X03533; CAA27234.1; -
 DR EMBL: X03533; CAA27235.1; ALT SEQ.
 DR EMBL: X03533; CAA27236.1; ALT SEQ.
 DR EMBL: M21511; AAA39422.1; ALT_SEQ.
 DR EMBL: M18098; AAA39421.1; -
 DR PIR: A23639; A23639.
 DR HSSP: P06239; ILCK.
 DR MGD: MGI:96736; LCK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SMO0252; SH2; 1.

DR SMART: SMO0326; SH3; 1.
 DR SMART: SMO0219; TYKIC; 1.
 DR PROSITE: P800107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: P800109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: P850011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: P850001; SH2; 1.
 DR PROSITE: P850002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferase;
 KW ATP-binding; Myristate; SH2 domain; SH3 domain; Palmitate;
 KW Lipoprotein.
 FT INIT MET 0 0 PROBABLE. (BY SIMILARITY).
 FT LIPID 1 1 MYRISTATE.
 FT LIPID 2 2 PALMITATE.
 FT LIPID 4 4 PALMITATE.
 FT DOMAIN 60 120 SH3.
 FT DOMAIN 126 223 SH2.
 FT DOMAIN 126 223 SH2.
 FT NP BIND 244 497 PROTEIN KINASE.
 FT BINDING 250 256 ATP (BY SIMILARITY).
 FT ACT SITE 272 272 ATP (BY SIMILARITY).
 FT MOD RES 363 363 BY SIMILARITY.
 FT MOD RES 393 393 PHOSPHORYLATION (NEGATIVE REGULATION) (BY
 FT MOD RES 504 504 SIMILARITY).
 FT NOTAGEN 268 268 K->N: REDUCED ACTIVITY.
 FT NOTAGEN 269 269 V->L: REDUCED ACTIVITY.
 FT NOTAGEN 270 270 A->S: REDUCED ACTIVITY.
 FT NOTAGEN 271 271 V->A: REDUCED ACTIVITY.
 FT NOTAGEN 272 272 K->R: LOSS OF ACTIVITY.
 FT NOTAGEN 273 272 S->N: REDUCED ACTIVITY.
 FT NOTAGEN 274 274 L->M: REDUCED ACTIVITY.
 FT NOTAGEN 275 275 K->V: REDUCED ACTIVITY.
 FT NOTAGEN 504 504 Y->F: CAUSES THYMIC TUMORS.
 FT CONFLICT 282 283 VP -> DA (IN REF. 2).
 SQ SEQUENCE 508 AA; 57821 MW; B92562498CA6878 CRC64;
 Query Match 50.9%; Score 227; DB 1; Length 508;
 Best Local Similarity 54.2%; Pred. No. 2.7e-15;
 Matches 45; Conservative 12; Mismatches 26; Indels 0; Gaps 0;
 Qy 1 MYEGLSREKAKELLPLPQNGAFRLRESQTRGSYSVLSRPAWDRIRHRIHCL 60
 Db 126 WFFKXLSKDAERQLAPGNTGSLFIRESESTRGSFSLVDFDQNGVGVHYRNL 185
 Qy 61 DNGMVLISPRITFSPGLALVDHY 83
 Db 186 DNGGFYISPRITFPGHLVDYHY 208
 RESULT 11
 BLK_MOUSE STANDARD; PRT; 498 AA.
 ID BLK_MOUSE
 AC P16277;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-
 DE BLK).
 GN BLK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=90117147; PubMed=2404338;
 RA Dymecki S.M., Niederhuber J.E., Desiderio S.V.;
 RT "Specific expression of a tyrosine kinase gene, blk, in B lymphoid
 RT cells.";
 RL Science 247:332-336(1990).
 RN [2]
 RP STRUCTURE BY NMR OF SH2 DOMAIN.
 RX MEDLINE=96224819; PubMed=8639560;

RA Metzler W.J., Leitling B., Pryor K., Mueller L., Farmer B.T. II.
 RT "The three-dimensional solution structure of the SH2 domain from
 RT p53blk kinase." Biochemistry 35:6201-6211(1996).
 CC -1- FUNCTION: BLK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT
 CC IS RESTRICTED TO B LYMPHOID CELLS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 DR EMBL/ M30903; AAA40453.1; -
 DR PIR/ A40092; A40092.
 DR PDB/ 1BLJ; 12-MAR-97.
 DR PDB/ 1BLK; 12-MAR-97.
 DR MGD/ MGT88169; BLK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam/ PF00017; SH2; 1.
 DR Pfam/ PF00018; SH3; 1.
 DR Pfam/ PF00069; pkinase; 1.
 DR PRINTS: PRO0401; SH2DOMAIN.
 DR PRINTS: PRO0452; SH3DOMAIN.
 DR PRINTS: PRO0109; TYRKINASE.
 DR ProDom/ PD000001; Euk_pkinase; 1.
 DR ProDom/ PD000066; SH3; 1.
 DR ProDom/ PD000093; SH2; 1.
 DR SMART/ SM00252; SH2; 1.
 DR SMART/ SM00326; SH3; 1.
 DR SMART/ SM00219; Tyrc; 1.
 DR PROSITE/ PS00107; PROTEIN KINASE_ATP; 1.
 DR PROSITE/ PS00109; PROTEIN KINASE_TYR; FALSE_NEG.
 DR PROSITE/ PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE/ PS50002; SH3; 1.
 DR PROSITE/ PS50002; SH2; 1.
 DR Tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding;
 KW Myristate; SH2 domain; SH3 domain; 3D-structure.
 FT INIT MET 0 0
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT DOMAIN 51 111 SH3.
 FT DOMAIN 117 213 SH2.
 FT DOMAIN 234 487 PROTEIN KINASE.
 FT NP BIND 240 248 ATP (BY SIMILARITY).
 FT BINDING 262 262 ATP (BY SIMILARITY).
 FT ACT SITE 353 353 BY SIMILARITY.
 FT MOD RES 382 382 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 498 AA; 56513 MW; BE49DB079FDD577 CRG44;
 Query Match 50.3%; Score 224.5; DB 1; Length 498;
 Best Local Similarity 51.8%; Pred. No. 5,3e-19;
 Matches 43; Conservative 16; Mismatches 23; Indels 1; Gaps 1;
 QY 1 WLYEGLSREKAEELLPLPGNGAFLLRSGOTRRGYSIVRLSPASMDRIRHYRHCL 60
 DB 117 WFFRTSRKDAERQGLLPANRKAQSFLLRSESNKGAFLSVK-DITQGEVYKHKISL 175
 QY 61 DNGWLITSPLRTPPSLOALVDHY 83
 DB 176 DNGGYISPRITPTLQALVQHY 198

RESULT 12
 LCK CHICK STANDARD; PRT; 507 AA.
 AC P42683;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase LCK (BC 2.7.1.112) (Protein-
 DE tyrosine kinase C-TKL).
 GN LCK.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 RN [1] NCBI TaxID=9031;
 RP SEQUENCE OF 1-68 FROM N.A.
 RX MEDLINE=92186854; PubMed=1545804;
 RA Chow L., Ratcliffe M., Veillette A.;
 RT "tkl is the avian homolog of the mammalian lck tyrosine protein
 RT kinase gene." Mol. Cell. Biol. 12:1226-1233(1992).
 RN [2]
 RP SEQUENCE OF 46-507 FROM N.A.
 RX MEDLINE=88097370; PubMed=3321053;
 RA Streibhardt K., Mullins J.T., Bruck C., Ruebsamen-Waigmann H.;
 RT "Additional member of the protein-tyrosine kinase family: the src-
 RT and lck-related protooncogene c-tkl." Proc. Natl. Acad. Sci. U.S.A. 94:8778-8782(1997).
 CC -1- FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER
 CC CD4 OR CD8.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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 DR EMBL/ M85043; AAA49003.1; -
 DR EMBL/ J03579; AAA49081.1; ALU_INIT.
 DR HSP/ P06239; 3LCK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam/ PF00017; SH2; 1.
 DR Pfam/ PF00018; SH3; 1.
 DR Pfam/ PF00069; pkinase; 1.
 DR PRINTS: PRO0401; SH2DOMAIN.
 DR PRINTS: PRO0452; SH3DOMAIN.
 DR PRINTS: PRO0109; TYRKINASE.
 DR ProDom/ PD000001; Euk_pkinase; 1.
 DR ProDom/ PD000066; SH3; 1.
 DR ProDom/ PD000093; SH2; 1.
 DR SMART/ SM00252; SH2; 1.
 DR SMART/ SM00326; SH3; 1.
 DR SMART/ SM00219; Tyrc; 1.
 DR PROSITE/ PS00107; PROTEIN KINASE_ATP; 1.
 DR PROSITE/ PS00109; PROTEIN KINASE_TYR; 1.
 DR PROSITE/ PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE/ PS50002; SH3; 1.
 DR PROSITE/ PS50002; SH2; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferase;
 ATP-binding; Myristate; SH2 domain; SH3 domain; Palmitate;

KM Lipoprotein. 0 0 PROBABLE. (BY SIMILARITY).
 FT INIT MET 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).
 FT LIPID 4 4 PALMITATE (BY SIMILARITY).
 FT DOMAIN 59 119 SH3.
 FT DOMAIN 125 222 SH2.
 FT DOMAIN 243 496 PROTEIN KINASE.
 FT NP BIND 249 257 ATP (BY SIMILARITY).
 FT BINDING 271 271 ATP (BY SIMILARITY).
 FT ACT SITE 362 362 BY SIMILARITY.
 FT MOD RES 392 392 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD RES 503 503 PHOSPHORYLATION (NEGATIVE REGULATION) (BY SIMILARITY).
 SQ SEQUENCE 507 AA; 5808 MW; BC83C4FA891B6170 CRC64;
 Query Match 50.0%; Score 223; DB 1; Length 507;
 Best Local Similarity 53.0%; Pred. No. 8.2e-19;
 Matches 44; Conservative 14; Mismatches 25; Indels 0; Gaps 0;
 QY 1 WLVEGLSRKAEELLPGNPGAFILRESQTRGYSLSVRLSPASMDRIHRIHCL 60
 DB 125 WPKNLSKKNARLNLASGHTSGFLRESQTSKYSLSVDPDQNGETVHYKIRNM 184
 QY 61 DNGWLYISPRLTFFPSLOALVDHY 83
 DB 185 DNGGYIISPRVTFSSLHELVY 207
 RESULT 13
 YES_XIPHE STANDARD; PRT; 544 AA.
 ID YES_XIPHE
 AC P27447;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase YES (EC 2.7.1.112) (P61-YES) (C-YES).
 GN YES.
 OS Xiphophorus helleri.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;
 OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
 NC NCB1_TaxID=8084;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rio Lancetilla;
 RX MEDLINE=91187435; PubMed=1707152;
 RA Hennig G., Ottillie S., Scharl M.;
 RT "Conservation of structure and expression of the c-yes and fyn genes in lower vertebrates";
 RT Oncogene 6:361-369(1991).
 RL OncoGene 6:361-369(1991).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL; X54970; CAA38714.1; -.
 DR HSSP; P12931; IFMK.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR01452; SH3.

DR InterPro; IPR01245; Tyr_pkinase.
 DR Pfam; P00017; SH2; 1.
 DR Pfam; P00018; SH3; 1.
 DR Pfam; P00069; pkinase; 1.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH2DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KM Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding; Myristate; SH3 domain; SH2 domain.
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 FT DOMAIN 92 153 SH3.
 FT DOMAIN 159 256 SH2.
 FT DOMAIN 278 531 PROTEIN KINASE.
 FT NP BIND 284 292 ATP (BY SIMILARITY).
 FT BINDING 306 306 ATP (BY SIMILARITY).
 FT ACT SITE 397 397 BY SIMILARITY.
 FT MOD RES 427 427 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 544 AA; 61288 MW; 7D4181B3E7086EF CRC64;
 Query Match 48.7%; Score 217; DB 1; Length 544;
 Best Local Similarity 54.2%; Pred. No. 4.6e-18;
 Matches 45; Conservative 9; Mismatches 29; Indels 0; Gaps 0;
 QY 1 WLVEGLSRKAEELLPGNPGAFILRESQTRGYSLSVRLSPASMDRIHRIHCL 60
 DB 159 WYFGLSRKQTERLLLPNGRGFTFLRESQTKAYSLSDWDDETKDGNCKHYKIRKL 218
 QY 61 DNGWLYISPRLTFFPSLOALVDHY 83
 DB 219 DNGGYITRTQPSLQMLVDHY 241
 RESULT 14
 YES_XENLA STANDARD; PRT; 537 AA.
 ID YES_XENLA
 AC P10536;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-JUL-1989 (Rel. 11, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase YES (EC 2.7.1.112) (P61-YES) (C-YES).
 GN YES.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae.
 OC Xenopodidae; Xenopus.
 NC NCB1_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=89296347; PubMed=2472592;
 RX Steele R.E., Irwin M.Y., Knudsen C.L., Collett J.W., Ferro J.B.;
 RT "The yes proto-oncogene is present in amphibians and contributes to the maternal RNA pool in the oocyte";
 RT Oncogene Res. 4:223-233(1989).
 RL OncoGene Res. 4:223-233(1989).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X14377; CAA32551.1; -.
DR PIR: S08517; S08517.
DR HSSP: P00523; 2PTK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR ProDom: PD000066; SH3; 1.
DR ProDom: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
KM Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
KW Transferrase; ATP-binding; Myristate; SH3 domain; SH2 domain.
FT LIPID 2 MYRISTATE (BY SIMILARITY).
FT DOMAIN 85 146 SH3.
FT DOMAIN 152 249 SH2.
FT NP BIND 271 524 PROTEIN_KINASE.
FT BINDING 277 285 ATP (BY SIMILARITY).
FT ACT SITE 299 299 ATP (BY SIMILARITY).
FT MOD_RES 420 420 PHOSPHORYLATION (AURO-) (BY SIMILARITY).
SQ SEQUENCE 537 AA; 60357 MW; PFE26F615940AC3B CRC64;

Query Match 48.2%; Score 215; DB 1; Length 537;
Best Local Similarity 50.0%; Pred. No. 7,8e-18;
Matches 44; Conservative 11; Mismatches 23; Indels 10; Gaps 2;

QY 1 WLYEGLSREKAEKELLIPQNGAFLIRSGTSYSLRSPASWDRIR-----HY 55
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 152 WYFGMKRKAERLLINPQNGRTFLVRESEITTKAYSLIR-----DWDVKGDNVGHY 206
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 56 RIHCLDNGMLYISPRITPESLQALVDHY 83
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 207 KIRKLDNGGYITTTAFQESLQKVKHY 234
: : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
YES CHICK STANDARD; PRT; 541 AA.
ID YES CHICK STANDARD; PRT; 541 AA.
AC P09324;
DT 01-MAR-1989 (Rel. 10; Created)
DT 01-MAR-1989 (Rel. 10; Last sequence update)
DT 15-JUN-2002 (Rel. 41; Last annotation update)
DE Proto-oncogene tyrosine-protein kinase YES (EC 2.7.1.112) (pe1-YES)
DE (C-YES).
GN YES.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN (1)
RP SEQUENCE FROM N.A.

RX MEDLINE=89041591; PubMed=3054816;
RA Sudol M., Kiehwetter C., Zhao Y.H., Dorai T., Wang L.H.,
RA Hanafusa H.;
RT "Nucleotide sequence of a cDNA for the chick yes proto-oncogene:
RT comparison with the viral yes gene.";
RL Nucleic Acids Res. 16:9876-9876(1988).
RN [2]
RP REVISION TO 232.
RA Sudol M.;
RL Submitted (NOV-1988) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Brain;
RA MEDLINE=89128204; PubMed=2464785;
RA Zheng X., Podel S., Sefton B.M., Kaplan P.L.;
RT "The sequence of chicken c-yes and pe1c-yes.";
RL Oncogene 4:99-104(1989).
RN [4]
RP SEQUENCE OF 396-451 FROM N.A.
RX MEDLINE=93096482; PubMed=1281306;
RA Marcelle C., Bichmann A.;
RT "Molecular cloning of a family of protein kinase genes expressed in
RT the avian embryo.";
RL Oncogene 7:2479-2487(1992).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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DR EMBL: X13207; CAA31595.1; -.
DR EMBL: X12461; CAA31002.1; -.
DR EMBL: X65695; CAA49365.1; -.
DR PIR: S03124; TVCHTS.
DR HSSP: P00523; 2PTK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR000980; SH2.
DR InterPro: IPR001452; SH3.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00017; SH2; 1.
DR Pfam: PF00018; SH3; 1.
DR PRINTS: PR00401; SH2DOMAIN.
DR PRINTS: PR00452; SH3DOMAIN.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR ProDom: PD000066; SH3; 1.
DR ProDom: PD000093; SH2; 1.
DR SMART: SM00252; SH2; 1.
DR SMART: SM00326; SH3; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS50001; SH2; 1.
DR PROSITE: PS50002; SH3; 1.
KM Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
KW Transferrase; ATP-binding; Myristate; SH3 domain; SH2 domain.
FT LIPID 2 MYRISTATE (BY SIMILARITY).
FT DOMAIN 89 150 SH3.
FT DOMAIN 156 253 SH2.
FT NP BIND 271 528 PROTEIN_KINASE.
FT BINDING 281 289 ATP (BY SIMILARITY).
FT ACT SITE 303 303 ATP (BY SIMILARITY).

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FT ACT SITE 394 394 BY SIMILARITY.
 FT MOD RES 424 424 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT CONFLICT 67 71 TPFGG -> IHPLR (IN REF. 3).
 FT CONFLICT 82 82 P -> Q (IN REF. 3).
 SQ SEQUENCE 541 AA; 60792 MW; BEA849CC7D1755AF CRC64;

Query Match 48.0%; Score 214; DB 1; Length 541;
 Best Local Similarity 50.0%; Pred. No. 1e-17; Indels 10; Gaps 2;

Matches 44; Conservative 11; Mismatches 23; Indels 10; Gaps 2;

Qy 1 WLYEGLSREKAEELLPLPGNPGGAFLIRESQTRRGYSLSVRLSRPASMDRIR-----HY 55
 Db 156 WYFGKMGKRDARLLNPGNGRGIPLVRESEETTKGATSLIR-----DWDEVRGDNVKKY 210
 Qy 56 RICHLDNGMLYISPRLLTFPSLQALVDHY 83
 Db 211 KIRKLDNGGYITTRAQFESLQKLVKKY 238

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 Job time : 6.52121 secs